

3135pt nat'l phases.ST25  
SEQUENCE LISTING

<110> Leone, Arturo  
Turco, Maria Caterina

<120> BAG3 nucleotide and protein sequences to be used in research, diagnostics and therapy for cell death-involving diseases

<130> 3135PT nat'l phases

<140> PCT/EP2002/014802

<141> 2002-12-30

<150> EP01830834.6

<151> 2001-12-28

<160> 18

<170> PatentIn version 3.1

<210> 1

<211> 2533

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (307)..(2034)

<223> Human BAG3 gene sequence

NCBI Pub Med Accession Number: XM\_055575

Homo sapiens BCL2-associated athanogene 3 (BAG3)

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gcccggcgcc ggcttcccgg acacgtcggc ggccggagagg ggcccacggc ggccggcccgg 240  
ccagagactc ggcgcccgga gccagcgccc cgcacccgcg cccagcgagg cagaccccaa 300  
cccagc atg agc gcc gcc acc cac tcg ccc atg atg cag gtg gcg tcc 348  
Met Ser Ala Ala Thr His Ser Pro Met Met Gln Val Ala Ser  
1 5 10  
ggc aac ggt gac cgc gac cct ttg ccc ccc gga tgg gag atc aag atc 396  
Gly Asn Gly Asp Arg Asp Pro Leu Pro Pro Gly Trp Glu Ile Lys Ile  
15 20 25 30  
gac ccg cag acc ggc tgg ccc ttc ttc gtg gac cac aac agc cgc acc 444  
Asp Pro Gln Thr Gly Trp Pro Phe Phe Val Asp His Asn Ser Arg Thr  
35 40 45  
act acg tgg aac gac ccg cgc gtg ccc tct gag ggc ccc aag gag act 492  
Thr Thr Trp Asn Asp Pro Arg Val Pro Ser Glu Gly Pro Lys Glu Thr  
50 55 60  
cca tcc tct gcc aat ggc cct tcc cgg gag ggc tct agg ctg ccg cct 540  
Pro Ser Ser Ala Asn Gly Pro Ser Arg Glu Gly Ser Arg Leu Pro Pro  
65 70 75  
gct agg gaa ggc cac cct gtg tac ccc cag ctg cga cca ggc tac att 588  
Ala Arg Glu Gly His Pro Val Tyr Pro Gln Leu Arg Pro Gly Tyr Ile  
80 85 90

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gca Ala	gca Ala	gcg Ala	gct Ala 130	cct Pro	cag Gln	agg Arg	tcc Ser	cag Gln 135	tca Ser	cct Pro	ctg Leu	cgg Arg	ggc Gly 140	atg Met	cca Pro	732
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tcc Ser	att Ile	ccg Pro	gtg Val 210	ata Ile	cac His	gag Glu	cag Gln	aac Asn 215	gtt Val	acc Thr	cgg Arg	cca Pro	gca Ala 220	gcc Ala	cag Gln	972
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ctc Leu	cac His	tcc Ser	ccc Pro 290	tcg Ser	ccc Pro	atc Ile	cgt Arg	gtg Val 295	cac His	acc Thr	gtg Val	gtc Val	gac Asp 300	agg Arg	cct Pro	1212
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ccc cct gct cca gtt cct tgt cct cct ccc agc cct ggc cct tct gct Pro Pro Ala Pro Val Pro Cys Pro Pro Pro Ser Pro Gly Pro Ser Ala	1452
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gcc agg aga gac ggt gtc agg aag gtt cag acc atc ttg gaa aaa ctt Ala Arg Arg Asp Gly Val Arg Lys Val Gln Thr Ile Leu Glu Lys Leu	1788
gaa cag aaa gcc att gat gtc cca ggt caa gtc cag gtc tat gaa ctc Glu Gln Lys Ala Ile Asp Val Pro Gly Gln Val Gln Val Tyr Glu Leu	1836
cag ccc agc aac ctt gaa gca gat cag cca ctg cag gca atc atg gag Gln Pro Ser Asn Leu Glu Ala Asp Gln Pro Leu Gln Ala Ile Met Glu	1884
atg ggt gcc gtg gca gca gac aag ggc aag aaa aat gct gga aat gca Met Gly Ala Val Ala Ala Asp Lys Gly Lys Lys Asn Ala Gly Asn Ala	1932
gaa gat ccc cac aca gaa acc cag cag cca gaa gcc aca gca gca gcg Glu Asp Pro His Thr Glu Thr Gln Gln Pro Glu Ala Thr Ala Ala Ala	1980
act tca aac ccc agc agc atg aca gac acc cct ggt aac cca gca gca Thr Ser Asn Pro Ser Ser Met Thr Asp Thr Pro Gly Asn Pro Ala Ala	2028
ccg tag cctctgccct gtaaaaatca gactcggaac cgatgtgtgc tttagggaat Pro	2084
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20 25 30

Gln Thr Gly Trp Pro Phe Phe Val Asp His Asn Ser Arg Thr Thr Thr  
35 40 45

Trp Asn Asp Pro Arg Val Pro Ser Glu Gly Pro Lys Glu Thr Pro Ser  
50 55 60

Ser Ala Asn Gly Pro Ser Arg Glu Gly Ser Arg Leu Pro Pro Ala Arg  
65 70 75 80

Glu Gly His Pro Val Tyr Pro Gln Leu Arg Pro Gly Tyr Ile Pro Ile  
85 90 95

Pro Val Leu His Glu Gly Ala Glu Asn Arg Gln Val His Pro Phe His  
100 105 110

Val Tyr Pro Gln Pro Gly Met Gln Arg Phe Arg Thr Glu Ala Ala Ala  
115 120 125

Ala Ala Pro Gln Arg Ser Gln Ser Pro Leu Arg Gly Met Pro Glu Thr  
130 135 140

Thr Gln Pro Asp Lys Gln Cys Gly Gln Val Ala Ala Ala Ala Ala Ala  
145 150 155 160

Gln Pro Pro Ala Ser His Gly Pro Glu Arg Ser Gln Ser Pro Ala Ala  
165 170 175

Ser Asp Cys Ser Ser Ser Ser Ser Ser Ala Ser Leu Pro Ser Ser Gly  
180 185 190

Arg Ser Ser Leu Gly Ser His Gln Leu Pro Arg Gly Tyr Ile Ser Ile  
195 200 205

Pro Val Ile His Glu Gln Asn Val Thr Arg Pro Ala Ala Gln Pro Ser  
210 215 220

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Phe His Gln Ala Gln Lys Thr His Tyr Pro Ala Gln Gln Gly Glu Tyr  
 225 230 235 240  
 Gln Thr His Gln Pro Val Tyr His Lys Ile Gln Gly Asp Asp Trp Glu  
 245 250 255  
 Pro Arg Pro Leu Arg Ala Ala Ser Pro Phe Arg Ser Ser Val Gln Gly  
 260 265 270  
 Ala Ser Ser Arg Glu Gly Ser Pro Ala Arg Ser Ser Thr Pro Leu His  
 275 280 285  
 Ser Pro Ser Pro Ile Arg Val His Thr Val Val Asp Arg Pro Gln Gln  
 290 295 300  
 Pro Met Thr His Arg Glu Thr Ala Pro Val Ser Gln Pro Glu Asn Lys  
 305 310 315 320  
 Pro Glu Ser Lys Pro Gly Pro Val Gly Pro Glu Leu Pro Pro Gly His  
 325 330 335  
 Ile Pro Ile Gln Val Ile Arg Lys Glu Val Asp Ser Lys Pro Val Ser  
 340 345 350  
 Gln Lys Pro Pro Pro Pro Ser Glu Lys Val Glu Val Lys Val Pro Pro  
 355 360 365  
 Ala Pro Val Pro Cys Pro Pro Pro Ser Pro Gly Pro Ser Ala Val Pro  
 370 375 380  
 Ser Ser Pro Lys Ser Val Ala Thr Glu Glu Arg Ala Ala Pro Ser Thr  
 385 390 395 400  
 Ala Pro Ala Glu Ala Thr Pro Pro Lys Pro Gly Glu Ala Glu Ala Pro  
 405 410 415  
 Pro Lys His Pro Gly Val Leu Lys Val Glu Ala Ile Leu Glu Lys Val  
 420 425 430  
 Gln Gly Leu Glu Gln Ala Val Asp Asn Phe Glu Gly Lys Lys Thr Asp  
 435 440 445  
 Lys Lys Tyr Leu Met Ile Glu Glu Tyr Leu Thr Lys Glu Leu Leu Ala  
 450 455 460  
 Leu Asp Ser Val Asp Pro Glu Gly Arg Ala Asp Val Arg Gln Ala Arg  
 465 470 475 480  
 Arg Asp Gly Val Arg Lys Val Gln Thr Ile Leu Glu Lys Leu Glu Gln  
 485 490 495

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Lys Ala Ile Asp Val Pro Gly Gln Val Gln Val Tyr Glu Leu Gln Pro  
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Ser Asn Leu Glu Ala Asp Gln Pro Leu Gln Ala Ile Met Glu Met Gly  
                   515                                  520                                  525

Ala Val Ala Ala Asp Lys Gly Lys Lys Asn Ala Gly Asn Ala Glu Asp  
                   530                                  535                                  540

Pro His Thr Glu Thr Gln Gln Pro Glu Ala Thr Ala Ala Ala Thr Ser  
                   545                                  550                                  555                                  560

Asn Pro Ser Ser Met Thr Asp Thr Pro Gly Asn Pro Ala Ala Pro  
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 <223> Specific sequence comprised inside BAG3 gene sequence

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 gcccggcgcc ggcttcccgg acacgtcggc ggcggagagg ggcccacggc ggcggccccg 240  
 ccagagactc ggcgcccgga gccagcgcgc cgcacccgcg cccagcggg cagaccccaa 300  
 cccagcatga gcgccgccac cactcgcgcc atgatgcagg tggcgctcgg caacggtgac 360

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Gly Asp Arg Asp Pro Leu Pro Pro Gly Trp Glu Ile Lys Ile Asp Pro  
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Gln Thr Gly  
                   35

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<210> 5  
 <211> 1105  
 <212> DNA  
 <213> Homo sapiens

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attcccattc ctgtgctcca tgaaggcgct gagaaccggc aggtgcaccc tttccatgtc      180
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gtggcagcgg cggcggcagc ccagcccca gcctccacg gacctgagcg gtcccagtct      360
ccagctgcct ctgactgctc atcctcatcc tcctcggcca gcctgccttc ctccggcagg      420
agcagcctgg gcagtcacca gctcccgagg ggtacatct ccattccggt gatacacgag      480
cagaacgtta cccggccagc agcccagccc tccttccacc aagcccagaa gacgcactac      540
ccagcgcagc aggggggagta ccagaccac cagcctgtgt accacaagat ccaggggggat      600
gactgggagc cccggcccct gcgggcggca tccccgttca ggtcatctgt ccaggggtgca      660
tcgagccggg agggctcacc agccaggagc agcacgccac tccactcccc ctgccccatc      720
cgtgtgcaca ccgtggtcga caggcctcag cagcccatga cccatcgaga aactgcacct      780
gtttcccagc ctgaaaacaa accagaaagt aagccaggcc cagttggacc agaactccct      840
cctggacaca tccaattca agtgatccgc aaagagggtg attctaaacc tgtttcccag      900
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cctcctccca gccctggccc ttctgctgtc ccctcttccc ccaagagtgt ggctacagaa     1020
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Ala Asn Gly Pro Ser Arg Glu Gly Ser Arg Leu Pro Pro Ala Arg Glu  
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Gly His Pro Val Tyr Pro Gln Leu Arg Pro Gly Tyr Ile Pro Ile Pro  
35 40 45

Val Leu His Glu Gly Ala Glu Asn Arg Gln Val His Pro Phe His Val  
50 55 60

Tyr Pro Gln Pro Gly Met Gln Arg Phe Arg Thr Glu Ala Ala Ala Ala  
65 70 75 80

Ala Pro Gln Arg Ser Gln Ser Pro Leu Arg Gly Met Pro Glu Thr Thr  
85 90 95

Gln Pro Asp Lys Gln Cys Gly Gln Val Ala Ala Ala Ala Ala Ala Gln  
100 105 110

Pro Pro Ala Ser His Gly Pro Glu Arg Ser Gln Ser Pro Ala Ala Ser  
115 120 125

Asp Cys Ser Ser Ser Ser Ser Ser Ala Ser Leu Pro Ser Ser Gly Arg  
130 135 140

Ser Ser Leu Gly Ser His Gln Leu Pro Arg Gly Tyr Ile Ser Ile Pro  
145 150 155 160

Val Ile His Glu Gln Asn Val Thr Arg Pro Ala Ala Gln Pro Ser Phe  
165 170 175

His Gln Ala Gln Lys Thr His Tyr Pro Ala Gln Gln Gly Glu Tyr Gln  
180 185 190

Thr His Gln Pro Val Tyr His Lys Ile Gln Gly Asp Asp Trp Glu Pro  
195 200 205

Arg Pro Leu Arg Ala Ala Ser Pro Phe Arg Ser Ser Val Gln Gly Ala  
210 215 220

Ser Ser Arg Glu Gly Ser Pro Ala Arg Ser Ser Thr Pro Leu His Ser  
225 230 235 240

Pro Ser Pro Ile Arg Val His Thr Val Val Asp Arg Pro Gln Gln Pro  
245 250 255

Met Thr His Arg Glu Thr Ala Pro Val Ser Gln Pro Glu Asn Lys Pro  
260 265 270

Glu Ser Lys Pro Gly Pro Val Gly Pro Glu Leu Pro Pro Gly His Ile  
275 280 285



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Pro Ile Gln Val Ile Arg Lys Glu Val Asp Ser Lys Pro Val Ser Gln  
290 295 300

Lys Pro Pro Pro Pro Ser Glu Lys Val Glu Val Lys Val Pro Pro Ala  
305 310 315 320

Pro Val Pro Cys Pro Pro Pro Ser Pro Gly Pro Ser Ala Val Pro Ser  
325 330 335

Ser Pro Lys Ser Val Ala Thr Glu Glu Arg Ala Ala Pro Ser Thr Ala  
340 345 350

Pro Ala Glu Ala Thr Pro Pro Lys Pro Gly Glu Ala Glu Ala Pro Pro  
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Lys His Pro Gly Val Leu Lys Val Glu Ala Ile Leu Glu Lys Val Gln  
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Gly Leu Glu Gln Ala Val Asp Asn Phe Glu Gly  
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gctggaaatg cagaagatcc ccacacagaa acccagcagc cagaagccac agcagcagcg 180  
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ttcagagact ttaagtcagt tggtttttat tagctgcttg gtatgcagta acttgggtgg 360  
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Met Glu Met Gly Ala Val Ala Ala Asp Lys Gly Lys Lys Asn Ala Gly  
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Asn Ala Glu Asp Pro His Thr Glu Thr Gln Gln Pro Glu Ala Thr Ala  
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Ala Ala Thr Ser Asn Pro Ser Ser Met Thr Asp Thr Pro Gly Asn Pro  
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Ala Ala Pro  
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Asp Arg Asp Pro Leu Pro Pro Gly Trp Glu Ile Lys Ile Asp Pro Gln  
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Asp Lys Gly Lys Lys Asn Ala Gly Asn Ala Glu Asp Pro His Thr  
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Asn Pro Ser Ser Met Thr Asp Thr Pro Gly Asn Pro Ala Ala Pro  
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